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A METHOD OF PROPHYLAXIS AND TREATMENT AND AGENTS USEFUL FOR SAME

FIELD OF THE INVENTION

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The present invention relates generally to a method for the prophylaxis and treatment of infection by microorganisms in biological environments from where the microorganisms acquire iron, heme or porphyrin, generally but not exclusively for growth. Particular biological environments contemplated by the present invention include but are not limited to vascular regions and cavities as well as mucosal membranes in animals including mammals, reptiles, amphibians and fish and in avian species as well as hooves of livestock animals. The method of the present invention involves interrupting, reducing or otherwise antagonizing the interaction between a microbial-derived polypeptide, such as but not limited to a polypeptide having cysteine proteinase activity, and a porphyrin-containing molecule such as heme. The present invention further provides agents useful in the prophylaxis and treatment of microbial infection of biological environments such as vascular regions and cavities including mucosal membranes as well as hooves involving microbial acquisition of iron, heme or porphyrin. Such agents are particularly useful as components in therapeutic compositions. Particularly important microbial infections targeted by the present invention involve infections in the oral cavity, nasopharynx, oropharynx, vagina and urethra in mammals such as humans. Other important microbial infections include infections of hooves in livestock animals such as sheep, cattle and goats.

BACKGROUND OF THE INVENTION

25 Bibliographic details of the publications numerically referred to in this specification are collected at the end of the description.

Proteinases are enzymes which hydrolyse peptide bonds in peptides, polypeptides and proteins. One particular group of proteinases, the endopeptidases, cleave bonds within the peptide chain with varying degrees of specificity for particular amino acyl residues. An example of an endopeptidase is a serine proteinase which is characterized by a catalytically active serine

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residue in its active centre. Another example is a cysteine proteinase (sometimes referred to as a thiol proteinase) which has free -SH groups in its active centre.

There is increasing evidence for the potential importance of proteinases in microbial infection.

- 5 This is particularly highlighted by the involvement of cysteine proteinases in periodontal disease pathology caused by the Gram negative microorganism, *Porphyromonas gingivalis*. This microorganism was formally known as *Bacteroides* sp.

- 10 Periodontal disease affects a majority of adults in varying degrees and is associated with significant systemic morbidity (1,1a) including dental infection and loss of teeth. *Porphyromonas gingivalis* is implicated as an important pathogen by its high incidence and relative levels in human disease (2,2a) and by its virulence in mono-infected animals (3,4). Virulence of *P. gingivalis* has been attributed to several components of the microorganism including fimbriae (5,6), short-chain volatile acids (7,8), lipopolysaccharide (9,10), collagenase
15 activity (11,12) and non-collagenolytic cysteine proteinase activity (13,14,15).

- Cysteine proteinases have a range of activities including affecting the remodelling of matrix proteins and disrupting the immune response by stimulating collagen-degrading activity of host cells (13,14,16), degrading fibronectin (17), inactivating interferon- α (19) and interleukins
20 (18,20), interfering with the complement cascade (21,22) and degrading immunoglobulins (23,24). Furthermore, clotting and vascular permeability mechanisms may be disturbed (15,25,26), fibrinogen may be degraded (15,27) and erythrocytes agglutinated and lysed (28,29) by cysteine proteinase activity.

- 25 A number of *P. gingivalis* cysteine proteinases described in several reports have been demonstrated to be antigenically related (14,30,31) to the products of three related genes (32,33). Cysteine proteinases from *P. gingivalis* are generally referred to as gingipains. Two major gingipains, Arg-gingipain (RgpA [formerly Arg-gingipain-1 or RGPA]) and Lys-gingipain (Kgp [formerly KGP]) [32], prefer proteinaceous substrates with an arginine or lysine
30 in the P1 position, respectively.

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The gingipains are expressed on the outer membrane of *P. gingivalis* and may also be released with residues or as soluble proteins (34,35,36). It has been proposed that *P. gingivalis* binds to hemoglobin *via* the gingipains (38).

- 5 The catalytic domains of RgpA and Kgp constitute approximately one third of the translated protein product. C-terminal to the catalytic domain, there are the following four domains: HA1, HA2, HA3 and HA4 which are highly homologous between RgpA and Kgp. These non-catalytic COOH-terminal domains have previously been named hemagglutinin (HA) domains because at least one was thought to participate in hemagglutination (30). Because all of the domains of
- 10 the gingipains are found together predominantly in loose, non-covalent associations with one another after hydrolytic separation (34,37), the gingipains appear to be multifunctional proteins for aggregating erythrocytes then lysing these cells to obtain hemoglobin for the acquisition of iron, heme and/or porphyrin.
- 15 *P. gingivalis* is implicated as a periodontal pathogen of central importance by its relative high levels of coincidence with periodontal disease (52,53) and by its virulence in mono-infected animals (54). Pathogenicity of this organism has been attributed to several components including short chain volatile acids and lipopolysaccharide and there is increasing evidence for the critical role of fimbriae and multi-domain proteinase-adhesion proteins, i.e. the gingipains.
- 20 Indirect mechanisms are also important since these proteases can subvert the control of the inflammatory response by degrading host control proteins leading to a tissue-destructive process (55).

- This fastidious Gram negative anaerobic bacterium has an essential requirement for exogenous porphyrin, i.e. it is a porphyrin auxotroph and lacks a number of enzymes normally involved in
- 25 porphyrin synthesis, including: glutamyl-tRNA reductase, porphobilinogen synthase, porphobilinogen deaminase, uroporphyrinogen III cosynthase, uroporphyrinogen decarboxylase, coporphyrinogen III oxidase, HemM or uroporphyrinogen III methylase. Porphyrins are critical in the function of the cytochromes of this organism and, therefore, in electron transfer related
- 30 to energy currency. It has been further proposed that iron porphyrins accumulated at the cell surface constitute an effective anti-oxidant shield (56) which could explain the relative

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resistance of the organism to hydrogen peroxide. Of note, the organism requires supplementation of porphyrin, even in complex growth media. Thus, iron-free protoporphyrin IX can replace the requirement for heme in media containing sufficient inorganic iron .

- 5 In the environment of the periodontium, it is accepted that there would be only trace concentrations of free heme. Hence, the apparent preferred source of both iron and porphyrin would be hemoglobin. Bleeding is a diagnostic feature of gingival inflammation and *P. gingivalis* can be implicated, as it has been shown to be highly competitive in utilizing hemoglobin as a source of both porphyrin and iron.

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- The elucidation of the molecular and biochemical mechanisms involved in key regulatory pathways, such as pathways involving the acquisition of iron, heme and porphyrin, is paramount in developing strategies for the control of disease. The inventors have now determined the molecular mechanism of HA2 domain binding to porphyrin-containing molecules such as
- 15 hemoglobin and in particular heme. The elucidation of the mechanisms underlying hemoglobin binding provides a means for the rational design of antagonists to prevent, reduce or otherwise retard the growth and maintenance of microorganisms which require exogenous iron, heme or porphyrin.

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SUMMARY OF THE INVENTION

Nucleotide and amino acid sequences are referred to by a sequence identifier, i.e. <400>1, <400>2, etc. A sequence listing is provided after the claims.

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Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

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An aspect of the present invention contemplates a method for the prophylaxis or treatment of infection by a microorganism in a biological environment from where the microorganism acquires iron, heme or porphyrin, said method comprising administering to said environment an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule present in said biological environment.

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Another aspect of the present invention provides a method for the prophylaxis or treatment of infection by a microorganism in a mammal from where the microorganism acquires iron, heme or porphyrin, said method comprising administering to said environment an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

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Still another aspect of the present invention provides a method for the prophylaxis or treatment of infection by a microorganism in a mammal, said microorganism being substantially incapable of synthesizing porphyrins said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-

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binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

Yet another aspect of the present invention contemplates a method for prophylaxis or treatment of periodontal, pulmonary, vaginal, urethral or hoof disease resulting from infection by *P. gingivalis* or related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived molecule having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

Even still another aspect of the present invention contemplates a method for the prophylaxis or treatment of infection by a microorganism in a mammal, said microorganism substantially requiring exogenous iron, heme or porphyrin for growth or maintenance wherein said method comprises administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding moiety on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme and wherein said HA2 domain comprises:

- (i) an amino acid sequence substantially encoded by the nucleotide sequence set forth in <400>5 or a nucleotide sequence having at least about 40% similarity thereto or capable of hybridizing thereto under low stringency conditions; and/or
- (ii) an amino acid sequence substantially as set forth in <400>6 or an amino acid sequence having at least about 40% similarity thereto or at least about 20% identity after optimum alignment with the same sequence;

wherein said amino acid sequence is capable of interacting with an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

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Even yet another aspect of the present invention provides a method for the prophylaxis or treatment of infection by a microorganism in a mammal, said microorganism substantially requiring exogenous iron, heme or porphyrin for growth or maintenance wherein said method comprises administering to said mammal an effective amount of an agent for a time and under
5 conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding moiety on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme and wherein said HA2 domain comprises:

- 10 (i) an amino acid sequence substantially encoded by the nucleotide sequence set forth in <400>5 or a nucleotide sequence having at least about 40% similarity thereto or capable of hybridizing thereto under low stringency conditions; and/or
- (ii) an amino acid sequence substantially as set forth in <400>6 or an amino acid sequence
15 having at least about 40% similarity thereto or at least about 20% identity after optimum alignment with the same sequence;

and wherein the HA2-binding motif comprises a moiety structurally or functionally homologous to substructure (Ic) of structure (I) below:

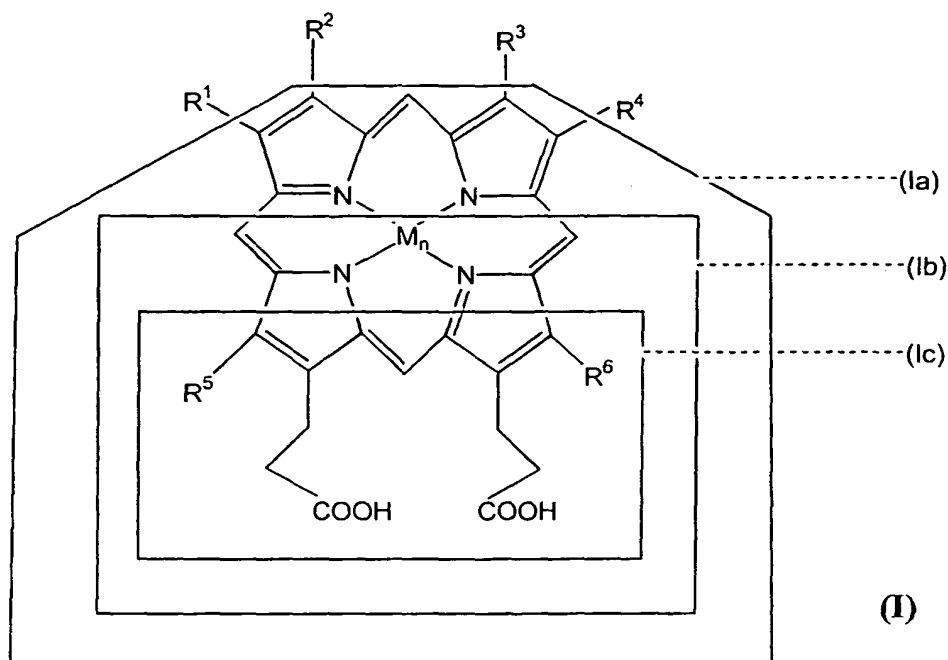
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Another aspect of the present invention contemplates a method for the prophylaxis or treatment of *P. gingivalis* infection or infection by a related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived HA2-containing molecule and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

Still another aspect of the present invention contemplates a method for the prophylaxis or treatment of *P. gingivalis* infection or infection by a related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived HA2-containing molecule comprising the amino acid sequence ALNPPNYLISKDVTG <400>1 or ALNPDNYLISKDVTGATKVKY <400>8 or an amino acid sequence having at least 40% similarity to <400>1 or <400>8 or at least about 20% identity after optimum alignment with same sequence or an amino acid sequence encoded by the nucleotide sequence <400>7 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridizing thereto under low stringency conditions and an HA2-binding motif comprising and

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including propionic acid groups or anionic or salt forms thereof such as but not limited to the region defined by substructure (Ic) in Formula (I) on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

- 5 Yet another aspect of the present invention provides an agent capable of antagonizing interaction between an HA2-containing molecule and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.
- 10 Even still another aspect of the present invention provides an agent capable of antagonizing interaction between an HA2-containing molecule and an HA2-binding motif on a porphyrin-containing molecule, said agent comprising propionic groups in planar alignment with respect to the molecular structure of said agent.
- 15 Even yet another aspect of the present invention provides a composition such as therapeutic or vaccine composition comprising an agent as herein before described and one or more pharmaceutically acceptable carriers and/or diluents.

A summary of the sequence identifiers referred to in the subject specification follows.

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SUMMARY OF SEQUENCE IDENTIFIERS

| Sequence | Sequence Identifier |
|--|----------------------------|
| Amino acid marker for HA2 binding (peptide #1) | <400>1 |
| Forward primer to amplify HA2 | <400>2 |
| Reverse primer to amplify HA2 | <400>3 |
| Amino acid sequence of peptide #2 | <400>4 |
| Nucleotide sequence encoding HA2 domain | <400>5 |
| Amino acid sequence of HA2 domain | <400>6 |
| Nucleotide sequence encoding <400>8 | <400>7 |
| Amino acid marker for HA2 binding (peptide #3) | <400>8 |

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a diagrammatic representation of the domain structure and homologies between the gingipains, RgpA and Kgp. CAT represents putative catalytic domain and HA represents putative hemagglutinin domains. Shaded areas represent regions of > 98% amino acid identity between the two gingipains. Fractions represent the degree of the identity for each RgpA domain.

Figure 2 is a graphical representation showing hemoglobin binding by rHA2, RgpA, and Kgp. (2a): Microtiter wells were coated with hemoglobin then incubated with 3 fold dilutions of purified rHA2, 2.5 $\mu\text{g/ml}$ (diamonds), RgpA, 5 $\mu\text{g/ml}$ (circles), or Kgp, 5 $\mu\text{g/ml}$ (triangles). Association of rHA2 with hemoglobin was measured with mAb 5A1 followed by substrate development at 414 nm after binding of secondary anti-mouse alkaline phosphatase-conjugated antibody. (2b): Hemoglobin binding by native but not denatured gingipains. Wells were coated with hemoglobin then incubated overnight with dilutions of either RgpA (closed circles), Kgp (closed triangles), or RgpA denatured by boiling (open circles) or Kgp denatured by boiling (open triangles). For this experiment, native or denatured gingipains that bound to hemoglobin were recognized with mAb IIB2, which specifically detects both native and denatured gingipains. Primary antibody IIB2 was followed by substrate development at 414 nm after binding of secondary anti-mouse AP-conjugated antibody. Data are representative of three separate experiments.

Figure 3 is a graphical representation showing binding of the HA2 domain to the heme moiety. (3a): Binding of rHA2 to dilutions of hemin (diamonds), hemoglobin (circles), or hemoglobin degraded by proteinase-K (triangles). Microtiter wells were coated with dilutions of samples then overnight binding of rHA2 to coated wells was detected with mAb 5A1 followed by substrate development at 414 nm after binding of secondary anti-mouse AP-conjugated antibody. The absence of contaminating protein within 90 μg of the hemin preparation and the absence of non-degraded subunits of hemoglobin remaining after proteinase-K treatment was verified by SDS-PAGE (data not shown). (3b): Binding of rHA2 to hemin. Microtiter wells were coated with hemin and overnight binding of rHA2 dilutions was detected with mAb 5A1

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as above. Data are representative of two separate experiments.

Figure 4 is a graphical representation showing inhibition of hemin- or hemoglobin-binding. Microtiter wells were coated overnight with hemin (panel a) or hemoglobin (panel b). rHA2
5 in *E. coli* lysate (100 fold dilution) (X), 65 ng/ml RgpA (circles) or 65ng/ml Kgp (triangles) were preincubated with dilutions of 300 μ M protoporphyrin IX for 1 hr then transferred to the ligand-coated plates for overnight incubation. Binding of rHA2 or the gingipains to coated wells was detected with mAb 5A1 or mAb IIB2, respectively, followed by substrate development at 414 nm after binding of secondary anti-mouse AP-conjugated antibody. Data are representative
10 of two separate experiments. The absence of contaminating protein in a 90 μ g protoporphyrin IX preparation was verified by SDS-PAGE and by Coomassie dye binding.

Figure 5 is a diagrammatic representation showing directed porphyrin-binding by rHA2. Microtiter wells were coated with 100 mM ethylene diamine (pH 4.7) then incubated with 90
15 μ g/ml hemin, protoporphyrin IX, or hematoporphyrin overnight in 50% dimethyl formamide in the presence (+) or absence (-) of 10 mM carbodiimide. Wells were washed 4 times with water then the amount of porphyrin bound to the wells was determined by absorbance at 414 nm (striped bars). Wells were blocked with PBS/Tween then incubated with 125 ng/ml rHA2 overnight. Binding of rHA2 to coated wells was detected with mAb 5A1 followed by substrate
20 development at 414 nm after binding of secondary anti-mouse AP-conjugated antibody (solid bars). Error bars represent standard deviation of absorbance measurements. Diagrams of chemical structures for hemin, protoporphyrin IX, and hematoporphyrin are presented adjacent to corresponding data.

Figure 6 is a graphical representation showing measurement of high-affinity binding of mAb 5A1 with rHA2 gingipains and gingipains from the culture supernatant. (6a): RgpA (circles), Kgp (triangles) or rHA2 in crude *E. coli* lysate (squares) were coated onto microtiter wells and incubated with serial dilutions of mAb 5A1. (6b): Dilutions of RgpA (open circles), Kgp (open triangles), or heat denatured RgpA (closed circles) or Kgp (closed triangles) were coated onto
25 microtiter wells with 3 fold dilutions from 10 μ g/ml then incubated with mAb 5A1. (6c): Purified rHA2 (squares) or purified high molecular-weight aggregates of gingipain domains
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isolated from culture supernatant (circles) were coated onto microtiter wells and incubated with serial dilutions of mAb 5A1. Data are representative of three separate experiments.

Figure 7 is a graphical representation showing immunoreactivity of synthetic peptides with mAb 5A1. ELISA demonstrating selective immunoreactivity of mAb 5A1 with peptide #1. Peptide #1 (squares) or peptide #2 (triangles) were coated onto microtiter plates at a concentration of 5 $\mu\text{g/ml}$ overnight then incubated with dilutions of mAb 5A1. Data are representative of two separate experiments.

Figure 8 is a graphical representation showing expression of HA2-related immunoreactive hemoglobin-binding protein from *P. gingivalis*. Aliquots of *P. gingivalis* culture medium were removed daily during a period of 8 d and immediately separated into a cell pellet and culture supernatant then frozen until use. OD^{660} and purity of the culture were measured daily. The cell pellets were dispersed evenly into 1 ml of PBS/ N_3 . (8a) and (8b): Arg- and Lys-specific proteinase activities, respectively, of the cell-free culture supernatant (squares) and cellular fraction (triangles) were measured as described. Measurements of the cellular fractions were normalized to culture densities (OD^{660}) recorded daily. (8c): The HA2 domain (1/243 dilution, open squares) and HA2 domain associated with hemoglobin-binding (1/81 dilution, solid squares) in culture supernatants were measured by ELISA and ligand binding assay, respectively, as described. In *P. gingivalis* whole cell fractions, the HA2 domain (1/243 dilution, open triangles) and HA2 domain associated with hemoglobin-binding (1/9 dilution, solid triangles) were measured by ELISA and ligand binding assay, respectively, as described. Measurements of the cell-associated fractions were normalized to culture densities (OD^{660}) recorded daily. Corresponding background immunoreactivity with a murine anti-human CD-19 IgG was subtracted from each measurement. Data are representative of two separate experiments in which patterns of expression were similar.

Figure 9 is a graphical representation of ligand binding to decreasing concentrations of rHA2. The ligands employed were: (a) deuteroporphyrin 1X 2,4 disulfonic acid (DDS); (b) deuteroporphyrin 1X 2,4 bisethylene glycol (DBEG); (c) dipyrrole 1 (C1; see Figure 10); (d) dipyrrole 2 (C2; see Figure 10); (e) dipyrrole 3 (C3; see Figure 10). Binding between the ligand

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and rHA2 was detected with monoclonal antibody (MAb) VAI followed by goat anti-mouse AP conjugate.

5 **Figure 10** is a diagrammatic representation of dipyrroles 1 (C1), 2 (C2) and 3 (C3) and the porphyrins protoporphyrin 1X (PPIX), deuteroporphyrin 1X 2,4 dihydrochloride (DDH), deuteroporphyrin 1X 2,4 disulfonic acid (DDS) and deuteroporphyrin 1X 2,4 bisethylene glycol (DBEG).

10 **Figure 11** is a graphical representation of showing competition between a ligand and hemoglobin (HG) for rHA2 binding. The ligands employed were: (a) protoporphyrin 1 X (PPIX); (b) deuteroporphyrin 1X 2,4 dihydrochloride (DDH); (c) deuteroporphyrin 1X 2,4 disulfonic acid (DDS); (d) deuteroporphyrin 1X 2,4 bisethylene glycol (DBEG); (e) dipyrrole 1 (C1; see Figure 10); (f) dipyrrole 2 (C2; see Figure 10) and (g) dipyrrole 3 (C3, see Figure 10).

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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

One aspect of the present invention contemplates a method for the prophylaxis or treatment of infection by a microorganism in a biological environment from where the microorganism
5 acquires iron, heme or porphyrin, said method comprising administering to said environment an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule present in said biological environment.

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The term "biological environment" is used in its broadest context to include an environment comprising porphyrin-containing molecules. Particularly preferred porphyrin-containing molecules include hemoglobin and its precursors as well as heme. Preferably, the biological environment is a vascular region or cavity or a mucosal membrane in an animal species such
15 as a mammal, reptile, amphibian, fish or bird or is a hoof of a livestock animal. More preferably, the animal is a mammal such as a human or livestock animal.

Accordingly, a preferred aspect of the present invention provides a method for the prophylaxis or treatment of infection by a microorganism in a mammal from where the microorganism
20 acquires iron, heme or porphyrin, said method comprising administering to said environment an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

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Although the present invention is particularly directed to *P. gingivalis* infection in the oral cavity such as during periodontal disease, it extends to any disease condition resulting from microbial infection and in particular infection by *P. gingivalis* or a related microorganism involving the acquisition of iron, heme or porphyrin. Such microorganisms are required to
30 acquire iron, heme or porphyrin as they do not possess a biosynthetic pathway for porphyrins. Examples of microorganisms related to *P. gingivalis* contemplated herein include but are not

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limited to *Salmonella sp.*, *Serratia sp.*, *Yersinia sp.*, *Klebsiella sp.*, *Vibrio sp.*, *Pseudomonas sp.*, *E. coli*, *Haemophilus sp.* and *Bordetella sp.* Examples of *P. gingivalis* or related microorganism infection contemplated by the present invention include infection of the oral cavity, nasopharynx, oropharynx, vagina and urethra as well as infection of mucosal membranes and
5 infection of hooves of livestock animals such as sheep, cattle and goats. An "effective" amount means a porphyrin-binding interfering effective amount, i.e. an amount sufficient to interfere with HA2 domain interaction with a porphyrin moiety.

Another aspect of the present invention provides a method for the prophylaxis or treatment of
10 infection by a microorganism in a mammal, said microorganism being substantially incapable of synthesizing porphyrins said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a
15 precursor form thereof or part thereof such as heme.

A related aspect of the present invention contemplates a method for prophylaxis or treatment of periodontal, pulmonary, vaginal, urethral or hoof disease resulting from infection by *P. gingivalis* or related microorganism in a mammal, said method comprising administering to said
20 mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived molecule having an HA2 domain and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

25 Reference herein to "*Porphyromonas gingivalis*" or its abbreviation "*P. gingivalis*" includes reference to all mutants, derivatives and variants of this organism as well as serological subtypes. The present invention further extends to microorganisms related to *P. gingivalis* at the metabolic, structural, biochemical, immunological and/or disease causing levels. Examples of related microorganisms are those listed above.

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The term "HA2" domain is used in its broadest context and includes regions having structural

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or functional homology to the HA2 region. An HA2 domain comprises a sequence of amino acids having conformationally and/or linearly defined binding capacity to an HA2-binding motif on a porphyrin containing molecule such as hemoglobin and more particularly heme.

- 5 A particularly preferred HA2 domain comprises the following amino acid sequence:

Ala Asp Phe Thr Glu Thr Phe Glu Ser Ser Thr His Gly Glu Ala Pro
 Ala Glu Trp Thr Thr Ile Asp Ala Asp Gly Asp Gly Glu Gly Trp Leu
 Cys Leu Ser Ser Gly Gln Leu Asp Trp Leu Thr Ala His Gly Gly Thr
 10 Asn Val Val Ser Ser Phe Ser Trp Asn Gly Met Ala Leu Asn Pro Asp
 Asn Tyr Leu Ile Ser Lys Asp Val Thr Gly Ala Thr Lys Val Lys Tyr
 Tyr Tyr Pro Val Asn Asp Gly Phe Pro Gly Asp His Tyr Ala Val Met
 Ile Ser Lys Thr Gly Thr Asn Ala Gly Asp Phe Thr Val Val Phe Glu
 Glu Thr Pro Asn Gly Ile Asn Lys Gly Gly Ala Arg Phe Gly Leu Ser
 15 Thr Glu Ala Asn Gly Ala (<400>6)

or a sequence having at least about 40% similarity to at least about 10 contiguous amino acids thereof or at least about 20% identity after optimum alignment with the same sequence.

Alternative percentage similarities include at least about 50% or 60% or 70% or 80% or 90%

- 20 or above. Alternative percentage identities include at least about 25% or 30%, 40%, 50%, 60%, 70%, 80% or 90% or above. An HA2 domain is also conveniently defined by being encoded by a sequence of nucleotides comprising the following sequence:

gca gac ttc acg gaa acg ttc gag tct tct act cat gga gag gca cca
 25 gcg gaa tgg act act atc gat gcc gat ggc gat ggt gag ggt tgg ctc
 tgt ctg tct tcc gga caa ttg gac tgg ctc aca gct cat ggc ggc acc
 aac gta gta agc tct ttc tca tgg aat gga atg gct ttg aat cct gat
 aac tat ctc atc tca aag gat gtt aca ggc gca acg aag gta aag tac
 tac tat cca gtc aac gac ggt ttt ccc ggg gat cac tat gcg gtg atg
 30 atc tcc aag acg ggc acg aac gcc gga gac ttc acg gtt gtt ttc gaa
 gaa acg cct aac gga ata aat aag ggc gga gca aga ttc ggt ctt tcc
 acg gaa gcc aat ggc gcc (<400>5)

or a nucleotide sequence having at least 40% similarity to at least about 30 contiguous
 35 nucleotides thereof or a nucleotide sequence capable of hybridizing thereto under low stringency conditions. Alternative percentage similarities include at least about 50% or 60%, 70%, 80%

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or 90% or above.

Accordingly, another aspect of the present invention contemplates a method for the prophylaxis or treatment of infection by a microorganism in a mammal, said microorganism substantially requiring exogenous iron, heme or porphyrin for growth or maintenance wherein said method comprises administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding moiety on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme and wherein said HA2 domain comprises:

- (i) an amino acid sequence substantially encoded by the nucleotide sequence set forth in <400>5 or a nucleotide sequence having at least about 40% similarity thereto or capable of hybridizing thereto under low stringency conditions; and/or
 - (ii) an amino acid sequence substantially as set forth in <400>6 or an amino acid sequence having at least about 40% similarity thereto or at least about 20% identity after optimum alignment with the same sequence;
- wherein said amino acid sequence is capable of interacting with an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

Preferred molecules having an HA2 domain include cysteine proteinases such as gingipains, a product of the *hagA* gene and any TonB dependent protein carrying an HA2 domain and in particular those TonB dependent proteins involved in the acquisition of heme. An example of a TonB-dependent protein is Tla (TonB-linked adhesin) (44). The present invention, however, extends to all HA2-containing molecules.

The term "infection" is used in its most general sense and includes the presence or growth of *P. gingivalis* or related microorganism resulting in a disease condition or having the capacity to

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result in a disease condition. The term "infection" further encompasses *P. gingivalis* or related microorganism when present as part of the normal flora. Such bacteria may, under certain circumstances, be responsible for disease development. Prophylaxis is contemplated in accordance with the present invention to reduce the levels of *P. gingivalis* or related
5 microorganism or to reduce the likelihood of a disease condition developing resulting from infection by *P. gingivalis* or a relative thereof.

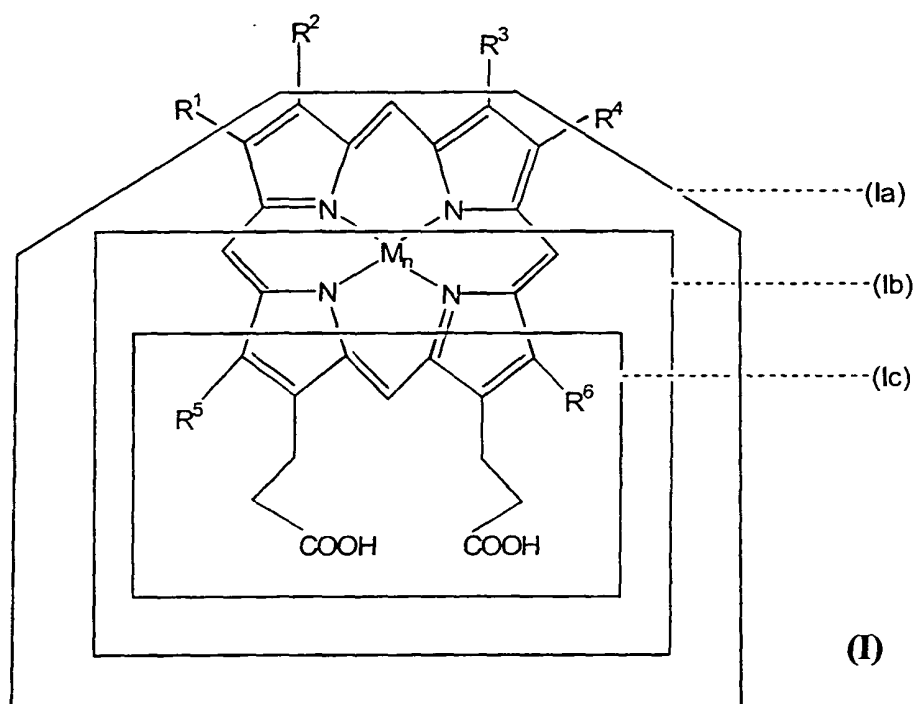
The present invention is particularly directed to the treatment of *P. gingivalis* or a related microorganism in humans. The present invention extends, however, to the prophylaxis or
10 treatment of *P. gingivalis* or related microorganisms in other mammals such as primates, livestock animals (e.g. sheep, cows, goats, pigs, horses, donkeys), companion animals (e.g. dogs, cats), laboratory test animals (e.g. mice, rats, guinea pigs, rabbits, hamsters) and captured wild animals.

15 In accordance with the present invention, it has been determined that the HA2 domain binds to a portion of the porphyrin moiety on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme. Preferably, the HA2 domain interacts with a surface exposed heme moiety of hemoglobin.

20 In a particularly preferred embodiment, the HA2 region interacts with the region on porphyrin, and in particular heme, comprising exposed propionic groups or their anionic or salt forms.

A porphyrin molecule is considered to have the structure shown in (I):

- 20 -



wherein R_1 and R_6 are the same or different and each is an alkyl such as a methyl, ethyl or propyl group, or hydrogen, hydroxyl, carboxyl, aldehyde, acetaldehyde or keto group, M is a metal ion in various oxidation states such as but not limited to Fe , Fe^{++} and Fe^{+++} and is optionally present such that n is 0 or 1. A person skilled in the art will appreciate that when n is 0, the trivalency of the two sp^3 hybridized N atoms will be completed by a hydrogen atom.

It is proposed in accordance with the present invention that the HA2-binding motif comprises the molecule defined by structure (I). Preferably, the HA2-binding motif comprises the region in substructure (Ic). More preferably, the HA2-binding motif comprises the region defined by substructure (Ib). Even more preferably, the HA2-binding motif comprises the region defined by substructure (Ia). Reference herein to the "HA2-binding motif" includes and comprises the motif defined by substructure (Ic), preferably substructure (Ib) and more preferably substructure (Ia) or a structurally or functionally homologous region capable of interacting with the HA2 domain of a molecule such as but not limited to a cysteine proteinase.

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Accordingly, another aspect of the present invention provides a method for the prophylaxis or treatment of infection by a microorganism in a mammal, said microorganism substantially requiring exogenous iron, heme or porphyrin for growth or maintenance wherein said method comprises administering to said mammal an effective amount of an agent for a time and under
5 conditions sufficient to antagonize the interaction between a molecule derived from said microorganism and having an HA2 domain and an HA2-binding moiety on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme and wherein said HA2 domain comprises:

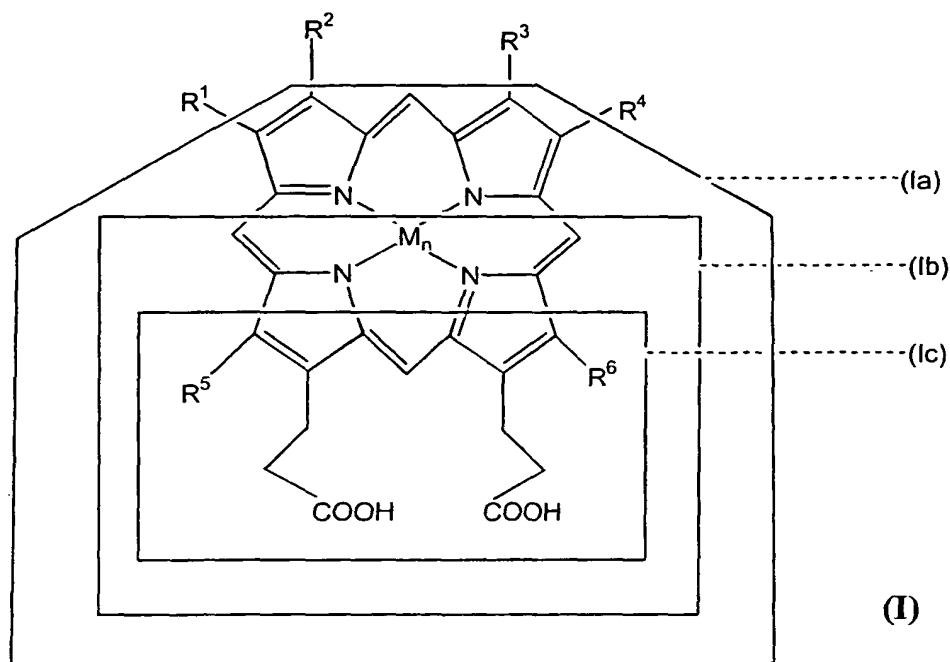
- 10 (i) an amino acid sequence substantially encoded by the nucleotide sequence set forth in <400>5 or a nucleotide sequence having at least about 40% similarity thereto or capable of hybridizing thereto under low stringency conditions; and/or
- (ii) an amino acid sequence substantially as set forth in <400>6 or an amino acid sequence
15 having at least about 40% similarity thereto or at least about 20% identity after optimum alignment with the same sequence;

and wherein the HA2-binding motif comprises a moiety structurally or functionally homologous to substructure (Ic) of structure (I) below:

20

25

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wherein R_1 and R_6 are the same or different and each is an alkyl such as a methyl, ethyl or propyl group, or hydrogen, hydroxyl, carboxyl, aldehyde, acetaldehyde or keto group, M is a metal ion in various oxidation states such as but not limited to Fe , Fe^{++} and Fe^{+++} and is optionally present such that n is 0 or 1.

Preferably, the HA2-binding motif comprises substructure (Ib). More preferably, the HA2-binding molecule comprises substructure (Ia).

10

Another aspect of the present invention contemplates a method for the prophylaxis or treatment of *P. gingivalis* infection or infection by a related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived HA2-containing molecule and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

15

Infection by *P. gingivalis* or related microorganism in accordance with this aspect of the present invention is one leading to or having the potential to lead to an infection of a mucosal or

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vascular region such in the oral cavity, nasopharynx, oropharynx, vagina or urethra as well as the hooves of farm animals.

Reference to a "*P. gingivalis*- derived HA2-containing molecule" includes gingipains bound to
5 *P. gingivalis* as well as soluble forms of the cysteine proteinase and the *hagA* gene product as well as TonB-dependent proteins such as the Tla protein (44).

The term "antagonize" means and includes reducing, inhibiting or otherwise adversely affecting interaction between the HA2 domain and that part of the porphyrin ring and in particular heme
10 which forms the HA2-binding motif on hemoglobin. The functional result of such antagonism is the inability or at least reduced capacity of *P. gingivalis* or related microorganism for acquiring iron, heme or porphyrin for use in, for example, metabolic pathways. Antagonism may be complete, i.e. from about 90-100% or partial, i.e. from about 20 to about 90% as determined by binding assays or inhibition of *P. gingivalis* growth or maintenance.

15 Although not intending to limit the present invention to any one theory or mode of action, it is proposed that *P. gingivalis* and its relatives do not have a complete functional porphyrin-synthesizing pathway and hence are porphyrin auxotrophs. In particular, it is proposed that *P. gingivalis* lacks one or more of a glutamyl-t RNA reductase, porphobilinogen synthase,
20 porphobilinogen deaminase, uroporphyrinogen III cosynthase, uroporphyrinogen decarboxylase, coproporphyrinogen III oxidase, HemM or uroporphyrinogen III methylase. As a result, *P. gingivalis* needs to acquire porphyrin for growth and/or maintenance or at least to facilitate growth and/or maintenance. Accordingly, by antagonizing the interaction between the HA2 domain and the HA2-binding motif the microorganism is unable to acquire porphyrin, iron or
25 heme and infection can be controlled.

In one embodiment, the antagonism results from inhibiting interaction between a region of surface exposed porphyrin and in particular heme comprising propionic acid groups or their anionic or salt forms such as but not limited to the region defined by sub-structure (Ic) and an
30 HA2 containing molecule comprising an epitope capable of interaction with monoclonal antibody mAb 5A1 (see ref 34). In accordance with the present invention, mAb 5A1 interacts

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with an epitope defined by amino acid sequence ALNPDNYLISKDVTG <400>1 or ALNPDNYLISKDVTGATKVKY <400>8 or an amino acid sequence having at least 40% similarity thereto or at least about 20% identity after optimum alignment with same sequence including an amino acid sequence defined by <400>1 or <400>8 but which has single or multiple amino acid substitutions, deletions and/or additions.

In an alternative embodiment, the HA2 containing molecule does not contain the mAb5A1 epitope.

10 The amino acid sequence defined by <400>1 or <400>8 is not the porphyrin binding site but a useful marker for HA2.

Accordingly, another aspect of the present invention contemplates a method for the prophylaxis or treatment of *P. gingivalis* infection or infection by a related microorganism in a mammal, said method comprising administering to said mammal an effective amount of an agent for a time and under conditions sufficient to antagonize the interaction between a *P. gingivalis*-derived HA2- containing molecule comprising the amino acid sequence ALNPPNYLISKDVTG <400>1 or ALNPDNYLISKDVTGATKVKY <400>8 or an amino acid sequence having at least 40% similarity to <400>1 or <400>8 or at least about 20% identity after optimum alignment with same sequence or an amino acid sequence encoded by the nucleotide sequence <400>7 or a nucleotide sequence having at least 40% similarity thereto or a nucleotide sequence capable of hybridizing thereto under low stringency conditions and an HA2-binding motif comprising and including propionic acid groups or anionic or salt forms thereof such as but not limited to the region defined by substructure (Ic) on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

The term "similarity" as used herein includes exact identity between compared sequences at the nucleotide or amino acid level. Where there is non-identity at the nucleotide level, "similarity" includes differences between sequences which result in different amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. Where there is non-identity at the amino acid level, "similarity" includes

- 25 -

amino acids that are nevertheless related to each other at the structural, functional, biochemical and/or conformational levels. In a particularly preferred embodiment, nucleotide and sequence comparisons are made at the level of identity rather than similarity.

5 Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include "reference sequence", "comparison window", "sequence similarity", "sequence identity", "percentage of sequence similarity", "percentage of sequence identity", "substantially similar" and "substantial identity". A "reference sequence" is at least 12 but frequently 15 to 18 and often at least 25 or above, such as 30 monomer units, inclusive of
10 nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (i.e. only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to
15 identify and compare local regions of sequence similarity. A "comparison window" refers to a conceptual segment of typically 12 contiguous residues that is compared to a reference sequence. The comparison window may comprise additions or deletions (i.e. gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for
20 aligning a comparison window may be conducted by computerized implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, WI, USA) or by inspection and the best alignment (i.e. resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be
25 made to the BLAST family of programs as for example disclosed by Altschul *et al.* (1997) (47). A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel *et al.* (1998) (48).

The terms "sequence similarity" and "sequence identity" as used herein refers to the extent that
30 sequences are identical or functionally or structurally similar on a nucleotide-by-nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. Thus, a "percentage of

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sequence identity", for example, is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g. A, T, C, G, I) or the identical amino acid residue (e.g. Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. For the purposes of the present invention, "sequence identity" will be understood to mean the "match percentage" calculated by the DNASIS computer program (Version 2.5 for windows; available from Hitachi Software engineering Co., Ltd., South San Francisco, California, USA) using standard defaults as used in the reference manual accompanying the software. Similar comments apply in relation to sequence similarity.

Reference herein to "similar" amino acids includes similarity at both the chemical and/or structural levels. Examples of similar amino acids based on chemical properties are as follows:-

| | | |
|-----------------|---|---|
| non-polar | - | Gly, Leu, Pro, Val, Ala, Met, Trp, Phe, Ile |
| polar uncharged | - | Ser, Asn, Gln, Thr, Cys, Tyr |
| acidic | - | Asp, Glu |
| basic | - | His, Lys, Arg. |

Examples of similar amino acids based on structural properties are as follows:-

| | | |
|---------|---|-----------------------------------|
| Group 1 | - | Asp, Asn, Glu, Gln, His |
| Group 2 | - | Tyr, Phe, Trp |
| Group 3 | - | Val, Pro, Cys, Ala, Thr, Ser, Gly |
| Group 4 | - | Arg, Lys |
| Group 5 | - | Met, Leu, Ile. |

In essence, amino acids which are similar include those which are observed in related proteins to be substituted by their partners at a higher frequency of the particular amino acid substitution

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as compared with random mutation (58).

Reference herein to a low stringency includes and encompasses from at least about 0 to at least about 15% v/v formamide and from at least about 1 M to at least about 2 M salt for hybridization, and at least about 1 M to at least about 2 M salt for washing conditions. Generally, low stringency is at from about 25-30°C to about 42°C. The temperature may be altered and higher temperatures used to replace formamide and/or to give alternative stringency conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5 M to at least about 0.9 M salt for hybridization, and at least about 0.5 M to at least about 0.9 M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01 M to at least about 0.15 M salt for hybridization, and at least about 0.01 M to at least about 0.15 M salt for washing conditions. In general, washing is carried out $T_m = 69.3 + 0.41 (G+C)\%$ (49). However, the T_m of a duplex DNA decreases by 1°C with every increase of 1% in the number of mismatch base pairs (50). Formamide is optional in these hybridization conditions. Accordingly, particularly preferred levels of stringency are defined as follows: low stringency is 6 x SSC buffer [SSC comprises sodium chloride and sodium citrate; 20 x SSC is prepared by dissolving 175.3 g of NaCl and 88.2 g of sodium citrate in 800 ml of H₂O; the pH is adjusted to 0.7 and the volume adjusted to 1 litre], 0.1% w/v sodium dodecyl sulphate (SDS) at 25-42°C; a moderate stringency is 2 x SSC buffer, 0.1% w/v SDS at a temperature in the range 20°C to 65°C; high stringency is 0.1 x SSC buffer, 0.1% w/v SDS at a temperature of at least 65°C. A salt is regarded as including any member of a class of compounds formed, together with water, by reaction of an acid with a base.

The identification of the molecular mechanism underlining HA2 interaction with hemoglobin provides a means for screening for antagonists of this interaction. Such antagonists are useful, for example, in the development of vaccines and therapeutic compositions for preventing or treating infection by *P. gingivalis* or related microorganisms.

Accordingly, another aspect of the present invention provides an agent capable of antagonizing

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interaction between an HA2-containing molecule and an HA2-binding motif on a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

- 5 Preferably, the agent antagonizes interaction between the HA2 containing molecule and a region on a porphyrin portion of hemoglobin comprising propionic acid groups or anionic or salt forms thereof.

Preferably, the region on hemoglobin is defined by substructure (Ic) as described above.

10

The agent may be a derivative of the HA2 containing molecule (e.g. gingipain or *hagA* gene product or Tla protein) or hemoglobin or may be identified following screening of a chemical library or following natural product screening. The latter includes screening of environments such as aquatic environments, coral, seabeds, microorganisms, plants and antarctic environments for naturally occurring molecules capable of acting as antagonists.

15

Alternatively, the HA2-containing molecule may be crystallized and antagonists derived based on the structure of the HA2 domain.

- 20 Any HA2-containing molecule such as the gingipain, *hagA* gene product or Tla protein or their derivatives may be used as vaccine components to generate antibodies to their HA2 domains or their immunological relatives. Alternatively, the antagonist may be an antibody to HA2 or an antibody to another region resulting in reduced binding of the HA2-containing molecule to hemoglobin. Antibodies may be employed from any source but may need to be humanized if
- 25 the intended use is in humans unless the antibodies are topically applied. Alternatively, the antibodies are raised by lactating dairy animals to provide passive immunization, particularly in the form of secretory antibody in dairy products.

- A range of potential antagonists may be identified from screening chemical libraries or
- 30 specifically designed for chemical synthesis. For example, the present invention extends to structural analogues of porphyrin or porphyrin-like molecules. In one embodiment, a nitrogen

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may replace any carbon especially in the Ic portion of the molecule. Alternatively, a molecule may be prepared as a dimer or trimer minimizing a porphyrin or porphyrin-like molecule. The multimerization may, for example, be complexing with a metal group. All such structural analogues may act as antagonists for HA2 interaction.

5

Furthermore, HA2-interaction antagonists may also be identified from a family of HA2-like molecules. In general, in addition to molecules having amino acid sequence similarity or identity, a family of proteins may be identified which have a tertiary structure which enables that molecule to interact with an HA2 domain in a manner analogous or functionally related to
10 known ligands of the HA2 domain. Proteins having a tertiary structure may differ at the amino acid identity level by up to 20%. Molecules may also be designed which retain tertiary functionality but differ at the amino acid level. Such molecules may be made by observing regions of the molecule which have a higher frequency of an amino acid substitution as compared with a random mutation. These particular substitutions may involve replacement by
15 chemically related amino acids in the sequence such as a hydrophobic amino acid for a hydrophobic amino acid or a basic amino acid for a basic amino acid. Generally, such substitutions would result with an amino acid similarity having a homology greater than four standard deviations above the control mean (57).

20 The antagonists, therefore, may be peptides, polypeptides, proteins, antibodies, small or large chemical entities or combinations thereof and may be in isolated, naturally occurring form or may be in recombinant or chemically synthetic form.

Screening for antagonists may be accomplished in any number of ways. In one method,
25 preparations of gingipains or HA2-containing parts thereof are incubated with potential antagonists and then subjected to chromatography or gel electrophoresis or immunoassay to screen for the formation of a complex.

In one particularly useful method, incubation mixtures of HA2-containing molecules and
30 potential antagonists are spotted onto porous chromatography paper and allowed to migrate through a portion previously impregnated with an antibody to the HA2. The aim of this method

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is to identify HA2-containing molecule-antagonist combinations which can no longer bind to the antibody. Identification of HA2-containing molecules whose migration is not retarded provides for a potential antagonist for binding to a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme. Antibody
5 mAb 5A1 may be used where more conformational antagonists are sought in the general HA2 region.

In addition to screening for suitable antagonists, the present invention enables the chemical synthesis and/or rational design for developing antagonists of HA2-porphyrin interaction. In
10 particular, data presented herein indicates that planarity of the propionic face of the porphyrin molecule is important for effective binding to HA2. The rational design of antagonists requires, therefore, developing a molecule in which the propionic face is aligned in a plane with respect to the molecule to which the propionic face forms part. Molecules and in particular antagonists with such conformation are encompassed by the present invention.

15 Accordingly, another aspect of the present invention provides an agent capable of antagonizing interaction between an HA2-containing molecule and an HA2-binding motif on a porphyrin-containing molecule, said agent comprising propionic groups in planar alignment with respect to the molecular structure of said agent.

20 There are many variations to the assays for screening for antagonists and all are encompassed by the present invention.

When the HA2-containing molecules or derivatives, analogues or homologues thereof are used
25 in a vaccine composition, they may be used as an immunogenic component to stimulate an immune response against the HA2 domain or they may be used as direct antagonists. They may also generate an immune response to other domains since this may cause conformational changes preventing HA2 interaction with a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme.

30 Accordingly, another aspect of the present invention provides a composition such as therapeutic

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or vaccine composition comprising an agent as hereinbefore described and one or more pharmaceutically acceptable carriers and/or diluents.

The immunogenic component of a vaccine composition as contemplated herein exhibits
5 excellent therapeutic activity, for example, in the prophylaxis and/or treatment of *P. gingivalis* infection when administered in an amount which depends on the particular case. For example, for recombinant peptide, polypeptide or protein molecules, from about 0.5 μ g to about 20 mg, may be administered, preferably from about 1 μ g to about 10 mg, more preferably from about
10 10 μ g to about 5 mg, and most preferably from about 50 μ g to about 1 mg equivalent of the immunogenic component in a volume of about 0.01 ml to about 5 ml or from about 0.1 ml to about 5 ml. The important feature is to administer sufficient immunogen to induce a protective immune response. The above amounts can be administered as stated or calculated per kilogram of body weight. Dosage regime can be adjusted to provide the optimum therapeutic response. For example, several divided doses can be administered or the dose can be proportionally
15 reduced as indicated by the exigencies of the therapeutic situation. Booster administration may also be required.

The vaccine of the present invention can further comprise one or more additional immunomodulatory components such as, for example, an adjuvant or cytokine molecule,
20 amongst others, which is capable of increasing the immune response against the immunogenic component. Non-limiting examples of adjuvants that can be used in the vaccine of the present invention include the RIBI adjuvant system (Ribi Inc., Hamilton, MT, USA), alum, mineral gels such as aluminium hydroxide gel, oil-in-water emulsions, water-in-oil emulsions such as, for example, Block co-polymer (CytRx, Atlanta GA, USA), QS-21 (Cambridge Biotech Inc.,
25 Cambridge MA, USA), SAF-M (Chiron, Emeryville CA, USA), AMPHIGEN[®] adjuvant, Freund's complete adjuvant; Freund's incomplete adjuvant; and Saponin, QuilA or other saponin fraction, monophosphoryl lipid A, and Avridine lipid-amine adjuvant. Other immunomodulatory agents that can be included in the vaccine include, for example, one or more cytokines, such as interferon and/or interleukin, or other known cytokines. Non-ionic surfactants such as, for
30 example, polyoxyethylene oleyl ether and n-hexadecyl polyethylene ether may also be included in the vaccines of the present invention.

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The vaccine composition can be administered in any convenient manner such as by oral, intravenous (where water soluble), intramuscular, subcutaneous, intranasal, intradermal or suppository routes or by implantation (e.g. using slow release technology). Depending on the route of administration, the immunogenic component may be required to be coated in a material to protect it from the action of enzymes, acids and other natural conditions which may inactivate it, such as those in the digestive tract.

The vaccine composition may also be administered parenterally or intraperitoneally. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof, or in oils. Under ordinary conditions of storage and use, these preparations can contain a preservative to prevent the growth of microorganisms. Alternatively, the vaccine composition can be stored in lyophilized form to be rehydrated with an appropriate vehicle or carrier prior to use.

Pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be fluid to the extent that easy syringeability exists, unless the pharmaceutical form is a solid or semi-solid such as when slow release technology is employed or it may be deliverable by spray, inhalation, nasal drip or microdroplets. In any event, it must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms.

The carrier may be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol and liquid polyethylene glycol, and the like), suitable mixtures thereof and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents such as, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal and the like. In many cases, it will be preferable to include isotonic agents such as, for example, sugars or sodium chloride. Prolonged

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absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption such as, for example, aluminum monostearate and gelatin.

5 Sterile injectable solutions are prepared by incorporating the active compound in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filter-sterilization. Generally, dispersions are prepared by incorporating the sterilized active ingredient into a sterile vehicle which contains the basic dispersion medium and the required other ingredients selected from those enumerated above. In the case of sterile
10 powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze-drying technique which yield a powder of the active ingredient plus any additional desired ingredient from previously sterile-filtered solution thereof.

Compositions comprising antagonists are formulated in a manner similar to transformation of an immunogenic composition.

15 The present invention extends to vaccine compositions which confer protection against infection by one or more isolates or sub-types of *P. gingivalis* including those that belong to the same serovar or serogroup as *P. gingivalis*. The vaccine composition preferably also confers protection against infection by other species of the genus *Prophyromonas* or other
20 microorganisms related thereto as determined at the nucleotide, biochemical, structural, physiological and/or immunointeractive level; the only requirement being that said other species or other microorganism produce a peptide, polypeptide or protein which is immunologically cross-reactive to an HA2-containing molecule of *P. gingivalis*. For example, such related
25 microorganisms may comprise genomic DNA which is at least about 70% similar overall to the genomic DNA of *P. gingivalis* as determined using standard genomic DNA hybridization and analysis techniques.

The terms "serogroup" and "serovar" relate to a classification of microorganisms which is based upon serological typing data, in particular data obtained using agglutination assays such as the
30 microscopic agglutination test (MAT). Those skilled in the art will be aware that serovar and serogroup antigens are a mosaic on the cell surface and, as a consequence there will be no strict

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delineation between bacteria belonging to a serovar and/or serogroup. Moreover, organisms which belong to different species may be classified into the same serovar or serogroup because they are indistinguishable by antigenic determination. As used herein, the term "serovar" means one or more *P. gingivalis* strains which are antigenically-identical with respect to antigenic determinants produced by one or more loci. Quantitatively, serovars may be differentiated from one another by cross-agglutination absorption techniques. As used herein, the term "serogroup" refers to a group of *Porphyromonas* spp. whose members cross-agglutinate with shared group antigens and do not cross-agglutinate with the members of other groups and, as a consequence, the members of a serogroup have more or less close antigenic relations with one another by simple cross-agglutination.

The present invention extends further to vaccine compositions capable of conferring protection against a "genetic variant" of *P. gingivalis*, the only requirement being that such a variant produce an HA2-containing peptide, polypeptide or protein capable of binding to an HA2-binding motif on a porphyrin-containing molecule. For example, the HA2-containing molecule may comprise at least about 40% similarity with respect to a *P. gingivalis* protein or at least about 20% identity after optimum alignment with same sequence.

The present invention further extends to combination vaccines comprising an effective amount of an immunogenic component of the present invention combined with an effective amount of one or more other antigens or therapeutic molecules capable of protecting the subject against other pathogens or disease conditions.

Particularly useful therapeutic compositions comprise antibodies to the porphyrin-binding motif of the HA2 domain or to other regions of the HA2 domain but which conformationally inhibits porphyrin binding.

The present invention further provides for the use of a gingipain or an HA2 domain containing part thereof or other HA2-containing molecule in the manufacture of a medicament for the prevention or treatment of infection by *P. gingivalis* or related microorganism.

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In a related aspect of the present invention, there is provided a use of an antagonist of interaction between a HA2-containing molecule from *P. gingivalis* or related microorganism and a porphyrin-containing molecule such as but not limited to hemoglobin or a precursor form thereof or part thereof such as heme in the manufacture of a medicament for the prophylaxis or
5 treatment of *P. gingivalis* infection.

The present invention is further described by the following non-limiting Examples.

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TABLE 1

| Amino Acid | Three-letter Abbreviation | One-letter Symbol |
|---------------|------------------------------|----------------------|
| Alanine | Ala | A |
| Arginine | Arg | R |
| Asparagine | Asn | N |
| Aspartic acid | Asp | D |
| Cysteine | Cys | C |
| Glutamine | Gln | Q |
| Glutamic acid | Glu | E |
| Glycine | Gly | G |
| Histidine | His | H |
| Isoleucine | Ile | I |
| Leucine | Leu | L |
| Lysine | Lys | K |
| Methionine | Met | M |
| Phenylalanine | Phe | F |
| Proline | Pro | P |
| Serine | Ser | S |
| Threonine | Thr | T |
| Tryptophan | Trp | W |
| Tyrosine | Tyr | Y |
| Valine | Val | V |
| Any residue | Xaa | X |

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EXAMPLE 1***RgpA and Kgp isolation***

Polydomain RgpA and Kgp were isolated and characterized as described (18) by Arginine-sepharose affinity chromatography of detergent-extracted *P. gingivalis* (ATCC 33277) cells. Alternatively, polydomain RgpA and Kgp were isolated as previously described (19) by arginine-Sepharose affinity chromatography from cell-free supernatant of a 10 d *P. gingivalis* batch culture.

EXAMPLE 2***Enzyme activity assays***

The proteinase activities of *P. gingivalis* culture fractions were measured using the substrates N-tertiary-butoxycarbonyl-Ile-Glu-Gly-Arg-7-amido-4-methylcoumarin or N-tertiary-butoxycarbonyl-Glu-Lys-Lys-7-amido-4-methylcoumarin at 30°C in Tris buffer without added reducing agents. Substrate hydrolysis was monitored over time by absorption at 460 nm using a 380 nm excitation beam on a Perkin Elmer LS 50B luminescence spectrophotometer.

EXAMPLE 3***Development of monoclonal antibodies 5A1 and IIB2***

Anti-gingipain monoclonal antibodies 5A1 and IIB2 were prepared in mice against gingipains as described (19).

EXAMPLE 4***Expression and purification of rHA2***

Forward and reverse primers (AACCTGCAGCGCGCAGACTTCACGG <400>2 and GGAAGCCAATGGCGCCAAAAGATCTAGT <400>3) were designed to amplify the HA2 domain from the *P. gingivalis* Arg-gingipain-1 proteinase gene (Accession Number U15282). Restriction sites for *Pst*I and *Bgl*II were designed into the 5' ends of the primers to facilitate

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cloning. Digested PCR product was ligated into the QIAexpressionist type III construct providing a 6x-His tag on the COOH-terminus (Qiagen Corp., USA). Transformation of the ligated construct was performed by electroporation into *E. coli* NM522 cells. *E. coli* cultures were grown at 37°C to an $OD^{600} = 0.6$ then induced with 0.1 mM isopropyl β -D-thiogalactopyranoside (IPTG) for 6 hours. Cells were harvested and resuspended to 5 ml per gram wet weight in buffer A (8 M Urea, 0.1 mM NaH_2PO_4 , 0.01 mM Tris-HCl, pH 7.9). The cells were stirred for 2 hrs at room temperature taking care to avoid foaming. This cell lysate was subjected to centrifugation at 31,000 g for 30 min at room temperature to pellet the cellular debris then the supernatant was subjected to ultracentrifugation at 130,000 g for 2 hrs. The clarified lysate was loaded onto a nickel-nitrilotriacetic acid column (Ni-NTA, Qiagen Corp., USA) pre-equilibrated with buffer A. The Ni-NTA column was washed with buffer A until baseline was reached. The protein was refolded on this column by running a linear gradient of urea from 8 M to 0 M in 20 mM Tris-HCl, 500 mM NaCl, 10% v/v glycerol, pH 7.9. The protein was then eluted with 50 mM Tris-HCl, 500 mM NaCl, 10% v/v glycerol, 250 mM imidazole, pH 7.9. The eluant was diluted 100 fold in 50 mM sodium acetate buffer, pH 5.5 and applied to a hemoglobin-agarose column pre-equilibrated with the dilution buffer. After loading, the column was washed with the same buffer until baseline was reached then the hemoglobin-binding protein was eluted with 50 mM Tris-HCl, pH 9. Protein concentrations were determined by Coomassie dye binding using bovine serum albumin as a standard.

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EXAMPLE 5

SDS-PAGE and Western blotting

SDS-PAGE was performed using 12% w/v gels with 4% w/v stackers by the method of Laemmli (39). All samples were diluted with SDS sample buffer before electrophoresis with (reducing) or without 2-mercaptoethanol. Western blots were performed by the method of Towbin (40) and proteins were transferred from the gels to polyvinylidene difluoride (PVDF) paper (BioRad Inc., CA, USA) with 300 mA for 1 hr. Blots were blocked with 0.1% w/v bovine serum albumin in 20 mM Tris-HCl with 500 mM NaCl containing 0.1% v/v Tween 20 (TBS/Tween). An alkaline phosphatase (AP) conjugate of a rabbit anti-mouse IgG (Dako Corp., USA) was used as a secondary antibody. Blots were washed with TBS/Tween between antibody

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applications. Substrate for AP was nitroblue tetrazolium in excess with 5-bromo-4-chloro-3-indoyl phosphate (NBT/BCIP) (BioRad, CA, USA) and color was developed in 5 mM Tris, pH 9.5.

- 5 NH₂-terminal amino acid sequencing of resolved SDS-PAGE proteins was performed as previously described (41).

EXAMPLE 6

ELISA

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Enzyme-linked immunosorbant assays (ELISA) were performed in polystyrene microtiter wells. Porphyrins and hemoglobin were used to coat the surfaces in 0.1 M NaOH or bicarbonate buffer pH 9 to determine optimal coating concentrations for saturation binding of rHA2. All wells were blocked and washed in PBS (2.7 mM KCl-1.5 mM KH₂PO₄-137 mM NaCl-8.1 mM Na₂HPO₄) with 10 mM NaN₃ and 0.1 % Tween 20 (PBS/Tween). Dilutions of rHA2 in 50mM acetate buffer pH 5.5 containing 137 mM NaCl, 0.1% Tween and 10mM NaN₃ (Acetate/Tween) were incubated overnight before washing in PBS/Tween. Primary murine monoclonal antibody (VA1) was applied in PBS/Tween at a concentration of 0.5 µg/ml for 1 hr at 37°C. Secondary goat anti-mouse antibodies conjugated with AP (Dako Corp.) were applied at a concentration of 1.1 µg/ml for 1 hr at 37°C, and then AP activity was monitored at 414 nm by hydrolysis of the substrate 4-nitrophenylphosphate (Boehringer GmbH, Mannheim, Germany) in 5 mM Tris (pH 9.5) by using a Titertek Twinreader PLUS photometer (absorbance maximum of 3.0 ELISA units). Mean apparent dissociation constants (K_{ds}) were derived by solid-phase ELISA as previously described (51).

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EXAMPLE 7

Ligand binding assay

The ligand-binding assay was a variant of the ELISA in which the ligand (i.e. hemoglobin, deuteroporphyrin 1X dihydrochloride, deuteroporphyrin 1X 2,4 bisethylene glycol, deuteroporphyrin 1X disulfonic acid and dipyrroles with varying placement of the propionate

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chains) that had been used to coat the wells in bicarbonate buffer or 0.1 M NaOH was subsequently allowed to bind to a second ligand-binding protein (i.e. rHA2) in Acetate/Tween or PBS/Tween. The ligand-binding protein was then detected with MAb VA1, followed by a goat anti-mouse AP conjugate, and developed as already described for ELISA. Bovine hemoglobin was used in these experiments. Deuteroporphyrin 1X 2,4 bisethylene glycol, deuteroporphyrin 1X dihydrochloride, deuteroporphyrin 1X disulfonic acid dihydrochloride, and dipyrroles tested were obtained from Porphyrin Products, Utah, USA.

HA2 domain was cloned, expressed and purified as a six-His tag fusion (51). Nucleic acid and NH₂-terminal amino acid sequencing verified the identities of the clone and the expression protein respectively, as the HA2 domain of RgpA.

EXAMPLE 8

Competition assay

The IC₅₀s for ligand binding in solution phase competition assays were determined. By using the standard ligand binding assay described herein, rHA2 at a concentration which produced 50% saturation binding to a hemoglobin-coated plate was preincubated for 1 hr in Acetate/Tween with dilutions of the porphyrins and then allowed to bind to hemoglobin-coated plates overnight. Hemoglobin was used as it was considered to represent the dominant form of porphyrin presentation in the pathological environment of chronic periodontitis.

EXAMPLE 9

Peptide synthesis

Peptides were synthesized by Chiron Mimotopes (Victoria, Australia) with terminal amines and carboxylic acids. Peptide #1 sequence was ALNPDNYLISKDVTG <400>1. Peptide #2 sequence was GEAPAEWTTIDADGDGQGWL <400>4. Peptide #3 is ALNPDNYLISKDVTGATKVKY <400>8. The latter amino acid sequence is encoded by the nucleotide sequence set forth in <400>7.

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EXAMPLE 10***Materials***

5 All chemicals and compounds were purchased from Sigma Corp., NSW, Australia unless otherwise herein specified.

EXAMPLE 11***Statistics***

10 Statistical differences of measurements between the gingipains and rHA2 were determined with one-tailed Student's t-tests.

EXAMPLE 12***Characteristics of RgpA and Kgp***

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The polydomain Lys-and Arg-gingipains (RgpA and Kgp, respectively) isolated from the CHAPS-extracted *P. gingivalis* cells possessed SDS-PAGE profiles, NH₂-terminal sequences, proteolytic activities and inhibition profiles characteristic of gingipain-like molecules previously described (19,34).

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The HA2 domain was cloned, expressed, and purified as a 6x His-tag fusion. Nucleic acid and NH₂-terminal amino acid sequencing verified the identity of the clone and the expressed protein, respectively, as the HA2 domain of RgpA.

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EXAMPLE 13***Hemoglobin is bound by rHA2 and by native but not denatured RgpA and Kgp***

30 Using the solid-phase ligand binding assay, rHA2, RgpA, and Kgp each bound to hemoglobin (Figure 2a). As mAb 5A1 was used to detect rHA2 bound to hemoglobin and did not interfere with this binding, it was evident that the epitope for mAb 5A1 within the HA2 domain was separate from the hemoglobin-binding site of HA2. Hemoglobin binding affinities were similar

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($P = 0.24$) for the rHA2, RgpA and Kgp ($K_d = 2.1 \pm 0.6$ nM) and the binding curves of neither the rHA2 nor the gingipains were indicative of multi-site binding (Figure 2a). High-affinity binding to hemoglobin at a single site within only the HA2 domain of both native RGPA and Kgp is sufficient to account for these observations. The binding site for hemoglobin within the gingipains appeared to be associated with higher-order protein structure since denaturation of RgpA and Kgp by boiling effectively eliminated their ability to bind hemoglobin (Figure 2b).

EXAMPLE 14

Hemoglobin binding of the HA2 domain is mediated through the heme moiety

To begin characterizing the binding between rHA2 and hemoglobin, the inventors examined the binding between rHA2 and hemin as well as binding to hemoglobin degraded by proteinase-K.

The rHA2 bound not only to wells coated with hemoglobin but also to wells coated with hemin or with the proteolytically degraded hemoglobin (Figure 3a). Binding of the rHA2 domain to hemin-coated wells was approximately 8 fold weaker than binding to hemoglobin in solid-phase assays ($K_d = 1.6 \pm 0.1 \times 10^{-8}$ M) (Figure 3b).

EXAMPLE 15

HA2 domain binds the porphyrin ring structure

To dissect the binding of the rHA2 domain to hemin, inhibition constants (IC_{50}) of the iron-free protoporphyrin IX in solution-phase competition assays were determined. Using the standard ligand binding assay described herein, rHA2 or the gingipains were preincubated with dilutions of protoporphyrin IX then allowed to bind to the hemin-coated wells. Binding of the gingipains or rHA2 to hemin was inhibited with the addition of protoporphyrin IX ($IC_{50} = 2.5 \pm 0.3$ μ M) (Figure 4a). IC_{50} values were similar between rHA2 and gingipains ($P = 0.42$). These data indicated that binding of rHA2 or the gingipains to hemin was specific for some aspect of the protoporphyrin ring. Importantly, binding of rHA2 or the gingipains to hemoglobin was also inhibited with protoporphyrin IX (Figure 4b) ($IC_{50} = 10 \pm 2$ μ M) and pre-incubation with the protoporphyrin could effectively eliminate binding to hemoglobin.

EXAMPLE 16

Directed protoporphyrin binding by recombinant HA2 (rHA2)

Examination of the hemoglobin crystal structure indicated that only the region of the heme moiety possessing the propionate functional groups (Figure 5) would be exposed for possible protein/protein contact. The inventors reasoned, therefore, that blocking access to the acidic region of protoporphyrin molecules would have an effect on rHA2-binding and allow more specific characterization of binding between the HA2 domain and the porphyrin ring. Modifying the ligand binding assay system used above, surfaces were first coated with ethylene diamine to provide fixed, free, primary amines for carbodiimide linkage of carboxylic acid groups. Hemin, protoporphyrin IX, and hematoporphyrin bound to wells coated with ethylene diamine with or without carbodiimide treatment as determined by absorbance at 414 nm (Figure 5, striped bars). rHA2-binding to the carbodiimide-treated porphyrins in the wells was almost eliminated, however, compared to the relatively greater association of the rHA2 with the non-derivatized porphyrins (Figure 5, solid bars). These data indicated that the rHA2 domain specifically recognized the three porphyrin compounds in the region of the propionic acid groups, as we were able to block rHA2-binding by directionally attaching the carboxylic acids of hemin, protoporphyrin IX, or hematoporphyrin to fixed amines. Since the heme moiety within hemoglobin is almost identical to these porphyrin molecules, the data suggested that the heme moiety of hemoglobin was bound by rHA2 and by the HA2 domain of the gingipains in a similar, directed, high-affinity manner.

EXAMPLE 17

*Epitope of mAb 5A1 is recognized in recombinant HA2 domain
and in RgpA and Kgp*

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In ELISA, mAb 5A1 bound to the rHA2 with a high affinity ($K_d = 2.2 \pm 0.5 \times 10^{-10}$ M) (Figure 6a). mAb 5A1 also bound to RgpA and Kgp isolated from the CHAPS-extracted *P. gingivalis* cells (Figure 6b). Soluble high molecular-weight aggregates of gingipain domains isolated from the cell-free fraction of a *P. gingivalis* batch culture by arginine-Sepharose affinity chromatography⁽³⁴⁾ were, however, recognized by mAb 5A1 ($K_d = 1.7 \pm 0.6 \times 10^{-10}$ M) (Figure 6c). Similarity of dissociation constants ($P = 0.36$) and of the binding curves suggested that

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mAb 5A1 recognized the same HA2 epitope in these polydomain gingipains as in rHA2.

EXAMPLE 18

*Epitope of mAb 5A1 is represented by an amino acid sequence
within the HA2 gingipain domain*

Using linear synthetic peptides, the epitope of mAb 5A1 was determined to be associated with the peptide ALNPDNYLISKDVTG <400>1 ($K_d = 3.8$ nM) which represents amino acids #1215-1229 of the translated Kgp within the HA2 domain (Figure 7, peptide #1). Dot blot analysis on PVDF membrane confirmed the unique immunoreactivity of this peptide with mAb 5A1. Similar results were obtained with peptide #3 (<400>8). A search of SwissProt database for the linear sequence of peptide #1 or GenBank database using the deduced nucleic acid sequence of this epitope resulted in no molecules with perfect homology to the peptide other than the gingipains and HagA, a large hemagglutinin with regions of identity to the entire HA2 domain.

EXAMPLE 19

*Correlation of HA2 domain immunoreactivity with hemoglobin
binding in P. gingivalis culture*

Detection of the HA2 epitope with mAb 5A1 in unfractionated *P. gingivalis* samples was correlated with hemoglobin binding. Because proteinase activity and gingipain expression have been shown to progressively change during the course of an extended *P. gingivalis* batch culture (34), the inventors examined cell-associated and extra-cellular fractions during 8 days of culture. Both Arg- and Lys-specific proteinase activities of the *P. gingivalis* cells peaked near the third day of culture (Figures 8a and b, triangles). Proteinase activities of the cell-free culture supernatants steadily rose throughout the culture period (Figures 8a and b, squares).

Immunoreactive protein in the cell-free conditioned culture medium detected with mAb 5A1 steadily accumulated throughout the 8 day culture period similar to proteolytic activity (Figure 8c, open squares). Immunoreactive protein associated with hemoglobin-binding in this supernatant fraction also increased steadily throughout the extended culture in a parallel manner

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(Figure 8c, closed squares). In the cellular fraction of the *P. gingivalis* culture, expression of immunoreactive protein increased early during the culture period with a peak near day 3 followed by a slight decrease then an increase to peak levels again by day 7, similar to proteolytic activity of this fraction (Figure 8c, open triangles). Immunoreactive protein associated with hemoglobin-binding in the cellular fraction followed a parallel pattern of expression (Figure 8c, closed triangles). These data demonstrated that detection of protein immunoreactive with mAb 5A1 in crude cellular and extra-cellular fractions of *P. gingivalis* culture was directly associated with hemoglobin-binding suggesting that mAb 5A1 specifically recognized the hemoglobin-binding, HA2 domain within *P. gingivalis* culture. Also, the data demonstrated a profile of HA2 domain expression and hemoglobin-binding activity similar with profiles of cellular and extra-cellular proteolytic activity expressed by *P. gingivalis*.

EXAMPLE 20

Controlling Porphyromonas gingivalis growth

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The control of *P. gingivalis* growth with prevention of periodontal pathology is achieved by interfering one or more pathways for obtaining heme. To this end, the inventors have shown that a monoclonal antibody recognizes an epitope within the hemoglobin-binding domain of the abundant *P. gingivalis* cysteine proteinases, i.e. gingipains, and have demonstrated increasing levels of this HA2 domain associated with hemoglobin-binding and proteinase activity in extended *P. gingivalis* culture. Further, the inventors have characterized the binding between the HA2 domain and hemoglobin suggesting that binding is mediated in large part through a specific recognition of the porphyrin ring of the heme moiety within the hemoglobin.

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Characterization of the binding between the recombinant HA2 (rHA2) domain and porphyrins allows for the design of efficient affinity ligands for purifying HA2, and allow structure-based design for heme/hemoglobin binding inhibitors. Heme acquisition is considered fundamental to the growth of *P. gingivalis*, and intervention with specific agents to disrupt pathways for heme-binding or uptake allows the control or prevention of periodontal disease.

EXAMPLE 21

Porphyromonas gingivalis does not contain a functional
porphyrin-biosynthetic pathway

- 5 The presence or absence of genetic sequences encoding enzymes required for porphyrin biosynthesis was assessed in *P. gingivalis*.

All entries for proteins used in the porphyrin biosynthesis pathway that are listed in the Swiss-Prot database (Release 37.0) were searched with TblastN against the available genomic data for
10 the *P. gingivalis* genome (45). This search comprized 257 eukaryotic, archaeal and prokaryotic protein sequences used in different pathways related to porphyrin biosynthesis. These are the standard enzymes in porphyrin biosynthesis, alternative enzymes used by subsets of organisms, the enzymes of the C₄ and C₅ pathways for 5-aminolevulinic acid synthesis, and enzymes used in Vitamin B₁₂ synthesis. Preliminary sequence data for *P. gingivalis* was obtained from The
15 Institute for Genomic Research through the website at <http://www.tigr.org>.

Open reading frames with some identity to enzymes required for heme synthesis were further examined by comparison with enzymes from four reference organisms: *Escherichia coli*, *Bacillus subtilis*, *Synechocystis* and *Aquifex aeolicus*, and the enzyme 5-aminolevulinic acid
20 synthase from *Bradyrhizobium japonicum*. Open reading frames were identified using the program Map and translated with Translate (46). Sequence identity between protein sequences was calculated using the program GAP and multiple alignments performed with PileUp (46).

Enzymes used solely in the pathway for vitamin B₁₂ synthesis were reported as a match if there
25 was an open reading frame (ORF) which has a BLAST score greater than 100. Enzymes and proteins involved in cytochrome synthesis were also BLAST searched against the genome. Proteins were aligned and identity calculated using GAP (46).

The proteins identified in Table 2 were BLAST searched against the *P. gingivalis* genome. No
30 significant matches were detected for the proteins glutamyl-tRNA reductase, porphobilinogen synthase, porphobilinogen deaminase, uroporphyrinogen III cosynthase, uroporphyrinogen

decarboxylase, coproporphyrinogen III oxidase, HemM or uroporphyrinogen III methylase.

The above observations indicate that *P. gingivalis* is unable to undergo *de novo* synthesis of porphyrin. Accordingly, the early and essential steps for synthesis of the tetrapyrrole ring are not encoded in the genome of *P. gingivalis*. As this organism has several proteins associated with tetrapyrrole rings, it is concluded that *P. gingivalis* has a requirement for porphyrin.

TABLE 2

Enzymes used in heme biosynthesis

| Enzyme | Function |
|----------------|---|
| Hem1/Hem0/HemA | 5-Aminolevulinic acid synthase |
| HemA/Hem1 | Glutamyl-tRNA reductase |
| HemB/Hem2 | Porphobilinogen synthase |
| HemC/Hem3 | Porphobilinogen deaminase |
| HemD/CysG/NasF | Uroporphyrinogen III cosynthase |
| HemE/DcuP | Uroporphyrinogen decarboxylase |
| HemF/Hem6 | Coproporphyrinogen III oxidase |
| HemH/HemZ | Ferrochelatase |
| HemL/HemK | Glutamate-1-semialdehyde 2, 1 aminotransferase |
| HemM | An enzyme in main pathway of synthesis of 5-aminolevulinate, possibly glutamyl-tRNA dehydrogenase |
| HemN | Oxygen-independent coproporphyrinogen III oxidase |
| HemX | Uroporphyrinogen III methylase |
| HemX | Protoporphyrinogen oxidase |
| GltX | Glutamyl-tRNA synthetase |

EXAMPLE 22***Clinical studies***

Patients presenting to a dental hospital were selected for a clinical study. The inclusion criteria were some level of adult periodontitis, no professional periodontal treatment within the prior three years nor use of antibiotics within the prior six months. Two donor sites, one relatively healthy and one with relatively advanced periodontal disease were selected in each mouth on the basis of radiographic examination. Clinical parameters were measured and plaque samples were obtained from each site. All periodontal samples and measurements were obtained by one of the inventors. Venous blood was collected within 30 min after plaque samples were obtained. Differences between categories were established by Student's 2-tailed t-test using 95% confidence levels. The relationships of values between categories were established by linear regression with a 95% confidence level. Levels of periodontal disease severity were assigned the following values: 0, none; 1, localized mild; 2, generalized mild; 3, localized moderate; 4, generalized moderate; 5, localized severe; 6, generalized severe.

Predictors of periodontal disease diagnosis such as pocket depths in sites of advanced disease, inflammation levels and attachment loss were relevant in this study (Pearson's correlation, $P = 0.038$, $P = 0.017$, $P < 0.001$, respectively).

The presence of the HA2 was defined by detection with the HA2-specific antibody mAb 5A1. Subgingival plaque samples collected from patients presenting for the first time for dental treatment were heat-denatured to maximize exposure of the HA2 domain and the epitope of mAb 5A1. Detection of the denatured HA2 domain with mAb 5A1 in plaque samples were more frequent in the relatively diseased donor sites than in the healthier donor sites (Student's t-test, $P = 0.004$). HA2 levels were positively associated with inflammation at the corresponding sites (linear regression, $P = 0.046$). The levels of HA2 were also strongly and positively associated with the amount of hemoglobin-binding activity that was measured from matched but non-denatured aliquots of these plaque samples (Pearson's correlation, $P < 0.001$).

The levels of the HA2 domain and levels of hemoglobin-binding activity measured in plaque

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samples from sites in the mouth were each positively associated with titres of serum IgG antibody specific for the rHA2 domain at the time of initial presentation ($P < 0.001$, $P = 0.007$, respectively). These data could be interpreted to indicate that lower HA2 levels in plaque and that either would predict lower HA2-specific IgG serum antibody levels in the patients at the
5 time of presentation. These data suggest that the HA2 domain is immunogenic in a human population eliciting a humoral IgG response in proportion to antigenic load.

Pre-therapy titres of serum antibody specific for the rHA2 domain (IgM, IgA and IgG combined) were found to be negatively correlated with the amount of lost tooth support (attachment loss)
10 at sites of advanced periodontitis (Pearson's correlation, $P = 0.33$). Pre-therapy antibody against HA2 domain was predominantly of the IgM isotype (Student's t-test, $P < 0.02$). Because loss of attachment is the greatest contributing factor in determining periodontal diagnosis and attachment loss was strongly correlated with periodontal diagnosis in this study (Pearson's correlation, $P < 0.001$), these data suggest that a lower serum antibody response to the HA2
15 domain would predict a greater level of clinical periodontal disease at the time of presentation. Conversely, the interpretation could be made that increasing the anti-HA2 antibody levels would be to protect against periodontal disease destruction.

Second samples of sera were collected some time after the commencement of periodontal
20 therapy to examine the possible inoculating effect that periodontal therapy might have on the host immune system. The commencement of treatment was significantly associated with an increase in IgG titre against the HA2 domain (Student's t-test, $P < 0.017$) with no change in the IgM or IgA titres. Correspondingly, pre-therapy and post-therapy anti-rHA2 IgG titres in patients were positively correlated ($P < 0.001$). Also, levels of HA2 domain in plaque at the time
25 of initial presentation were positively correlated with post-therapy rHA2-specific IgG titres ($P = 0.1$). These data strengthen evidence that the HA2 domain is immunogenic in a human population.

Importantly, serum antibody titres against the HA2 domain were correlated with serum antibody
30 titres against the whole *P. gingivalis* organism (Pearson's correlation, $P = 0.002$) implicating the HA2 domain as a significant extra-cellular antigenic constituent of *P. gingivalis* and a good

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candidate for immunologic targeting.

After the initiation of periodontal therapy, capacity for neutralization of hemoglobin-binding of the gingipains with IgG from post-treatment sera had become negatively associated with the diagnosis of periodontal disease severity (linear regression, RgpA, $P = 0.33$; Kgp, $P = 0.032$). Neutralization of hemoglobin-binding activity was confirmed to be IgG dependent by removing the neutralizing capacity of IgG fractions with a second pass over a protein-G affinity column. Taken together, these data suggest that a capacity to develop higher IgG titres against the HA2 domain of the gingipains may be associated with an increased functional antibody response in terms of hemoglobin-binding activity and protection against periodontal disease destruction.

EXAMPLE 23

Establishment of principles of porphyrin interaction

In the solid-phase ligand-binding assay, rHA2 bound to the porphyrins with similar binding affinities (Figure 9) showing that rHA2 was capable of binding to the propionic acid chains despite modification on the vinyl aspect. All the porphyrins tested were modified at the vinyl end to different degrees and the dipyrroles were half porphyrins with no vinyl moieties. The structures are shown in Figure 10. Despite these differences they all exhibited similar apparent K_d s of between 5-20 nM.

In the competition assay, only the dipyrroles were shown not to compete with hemoglobin for rHA2 (Figure 11). The apparent IC_{50} s for the deuteroporphyrins were again similar in value ranging from 3-8 μ M (Figure 11). This indicates that modification of the vinyl aspect did not affect the capacity of the porphyrins to compete for rHA2 as the IC_{50} s were comparable to that of protoporphyrin (PPIX). Of interest, the dipyrroles were incapable of competing with hemoglobin for rHA2 although they were capable of binding to rHA2 in the solid-phase assays. This is consistent with the non-planarity of free dipyrroles which is predictable based on their chemical structures. However, when bound to the plate, the dipyrroles are likely to be restrained and hence may present a propionic face as if were aligned in a plane. This implies that the planarity of the propionic face is important for effective competitive binding.

These results establish the key principles of the HA2 porphyrin interaction. These principles are necessary to guide the development of molecules that will compete efficiently *in vivo* for the HA2 moiety.

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Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, 10 individually or collectively, and any and all combinations of any two or more of said steps or features.

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